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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 13:10:08 EDT 2007

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Application No: 10797262 Version No: 2.1

Input Set:

Output Set:

Started: 2007-06-13 13:09:59.493
Finished: 2007-06-13 13:10:00.325
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 832 ms
Total Warnings: 9
Total Errors: 1
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

SEQUENCE LISTING

<110> East Tennessee State University Research Foundation
Lampson, Bert
Veloire, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10/797,262

<141> 2004-03-10

<160> 11

<170> PatentIn version 3.3

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

<400> 1

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1 5 10 15	

ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta	96
Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val	
20 25 30	

tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc	144
Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile	
35 40 45	

cgc gcc caa ctc ttg gcg gga acc tac cgg ccg gcg cct gtc cgc agg	192
Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg	
50 55 60	

gtc gga atc ccg aaa ccg ggc ggc ggc aca cgg cag cta ggc att ccc	240
Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro	
65 70 75 80	

acc gtg gtg gac cgg ctg atc caa caa gcc att ctt caa gaa ctc aca	288
Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr	
85 90 95	

ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg	336
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro	
100 105 110	

ggc cgt aac gcc cac gat gcc gtg cgg caa gcg caa ggc tac atc cag	384
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Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln	
115 120 125	
gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat	432
Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp	
130 135 140	
cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag	480
Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys	
145 150 155 160	
gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt	528
Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val	
165 170 175	
atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc	576
Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly	
180 185 190	
ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac	624
Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp	
195 200 205	
aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac	672
Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp	
210 215 220	
tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa	720
Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln	
225 230 235 240	
agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag	768
Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu	
245 250 255	
gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt	816
Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe	
260 265 270	
agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg	864
Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser	
275 280 285	
att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg	912
Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp	
290 295 300	
agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg	960
Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met	
305 310 315 320	
gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag	1008
Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln	
325 330 335	
acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt	1056
Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu	

340	345	350	
caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg			1104
Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly			
355	360	365	
ctg aaa gag aca gcg gtg atg gag atc gcc aat acc cga aaa gga gct			1152
Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala			
370	375	380	
tgg cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc			1200
Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr			
385	390	395	400
tac tgg acc gct caa ggg ctc aag agt ttg acg caa cga tat ttc gaa			1248
Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu			
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Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val			
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Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile			
35	40	45	
Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg			
50	55	60	
Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro			
65	70	75	80
Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr			
85	90	95	
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro			
100	105	110	

Gly	Arg	Asn	Ala	His	Asp	Ala	Val	Arg	Gln	Ala	Gln	Gly	Tyr	Ile	Gln	115	120	125	
Glu	Gly	Tyr	Arg	Tyr	Val	Val	Asp	Met	Asp	Leu	Glu	Lys	Phe	Phe	Asp	130	135	140	
Arg	Val	Asn	His	Asp	Ile	Leu	Met	Ser	Arg	Val	Ala	Arg	Lys	Val	Lys	145	150	155	160
Asp	Lys	Arg	Val	Leu	Lys	Leu	Ile	Arg	Ala	Tyr	Leu	Gln	Ala	Gly	Val	165	170	175	
Met	Ile	Glu	Gly	Val	Lys	Val	Gln	Thr	Glu	Glu	Gly	Thr	Pro	Gln	Gly	180	185	190	
Gly	Pro	Leu	Ser	Pro	Leu	Leu	Ala	Asn	Ile	Leu	Leu	Asp	Asp	Leu	Asp	195	200	205	
Lys	Glu	Leu	Glu	Lys	Arg	Gly	Leu	Lys	Phe	Cys	Arg	Tyr	Ala	Asp	Asp	210	215	220	
Cys	Asn	Ile	Tyr	Val	Lys	Ser	Leu	Arg	Ala	Gly	Gln	Arg	Val	Lys	Gln	225	230	235	240
Ser	Ile	Gln	Arg	Phe	Leu	Glu	Lys	Thr	Leu	Lys	Leu	Lys	Val	Asn	Glu	245	250	255	
Glu	Lys	Ser	Ala	Val	Asp	Arg	Pro	Trp	Lys	Arg	Ala	Phe	Leu	Gly	Phe	260	265	270	
Ser	Phe	Thr	Pro	Glu	Arg	Lys	Ala	Arg	Ile	Arg	Leu	Ala	Pro	Arg	Ser	275	280	285	
Ile	Gln	Arg	Leu	Lys	Gln	Arg	Ile	Arg	Gln	Leu	Thr	Asn	Pro	Asn	Trp	290	295	300	
Ser	Ile	Ser	Met	Pro	Glu	Arg	Ile	His	Arg	Val	Asn	Gln	Tyr	Val	Met	305	310	315	320
Gly	Trp	Ile	Gly	Tyr	Phe	Arg	Leu	Val	Glu	Thr	Pro	Ser	Val	Leu	Gln	325	330	335	

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
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Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
405 410 415

Leu Arg Gln Gly
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<213> Artificial

<220>
<223> Plasmid construct

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<221> misc_feature
<222> (1)..(1370)

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aacgcatctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaccaag 180
gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact 240
ggagcacgat ccgcgcccaa ctcttggcgg gaacctaccg gccggcgctt gtccgcaggg 300
tcggaatccc gaaaccgggc ggcggcacac ggcagctagg cattcccacc gtggtggacc 360
ggctgatcca acaagccatt cttcaagaac tcacacccat tttcgatcca gatttctccc 420
cttcagctt cggattccgt ccgggccgta acgcccacga tgccgtgcgg caagcgcaag 480
gtacatcca ggaagggtat cggtagctgg tcgacatgga cctggaaaag ttctttgatc 540

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gggtcaacca tgacatcttg atgagtcggg tggcccga aaacgcgtgc 600
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cggaggaagg gacgccgcaa ggcggccccc tcagccccct gctggcgaac atccttctcg 720
acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact 780
gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacggt 840
tcttgagaaa aacgctcaaa ctcaaagtaa acgaggagaa aagtgcgggtg gaccgcccgt 900
ggaaacgggc ctttctgggg tttagcttca caccggaacg aaaagcgcga atccggctcg 960
ccccaaggtc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga 1020
gcatatcgat gccagaacga attcatcgcg tcaatcaata cgtcatggga tggatcgggt 1080
atcttcggct cgtcgaaacc ccgtctgtcc ttcagaccat cgaaggatgg attcggagga 1140
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gagcgtggg gctgaaagag acagcgggtga tggagatcgc caatacccg aaaggagctt 1260
ggcgaacaac gaaaacgcc caactccacc aggccctggg caaacctac tggaccgctc 1320
aagggtcaa gagtttgacg caacgatatt tcgaactccg tcaaggttga 1370

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<210> 4
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Nucleotide primer containing NdeI restriction site

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<220>
<221> primer_bind
<222> (1)..(32)

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<210> 5
<211> 28
<212> DNA
<213> Artificial

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<220>
<223> Nucleotide primer containing BamHI restriction site

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<400> 5
aatggatccg ctggcgaaca tccttctc 28

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<210> 6
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<220>
<223> Nucleotide primer containing PstI restriction site

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<222> (1)..(29)

<400> 6
attactgcag agcgggtccag taggttttg 29

<210> 7
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<212> DNA
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<223> Nucleotide primer containing HindIII restriction site

<220>
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<222> (1)..(31)

<400> 7
actcaagctt gagaagggtc tgacgttcac g 31

<210> 8
<211> 455
<212> PRT
<213> Artificial

<220>
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<222> (1)..(455)

<220>
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<400> 8

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1 5 10 15

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35	40	45
Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile		
50	55	60
Asp Gly Val Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp		
65	70	75
Ser Thr Ile Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro		
85	90	95
Val Arg Arg Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu		
100	105	110
Gly Ile Pro Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln		
115	120	125
Glu Leu Thr Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly		
130	135	140
Phe Arg Pro Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly		
145	150	155
Tyr Ile Gln Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys		
165	170	175
Phe Phe Asp Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg		
180	185	190
Lys Val Lys Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln		
195	200	205
Ala Gly Val Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr		
210	215	220
Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp		
225	230	235
		240

Asp Leu Asp Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr
245 250 255

Ala Asp Asp Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg
260 265 270

Val Lys Gln Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys
275 280 285

Val Asn Glu Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe
290 295 300

Leu Gly Phe Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala
305 310 315 320

Pro Arg Ser Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn
325 330 335

Pro Asn Trp Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln
340 345 350

Tyr Val Met Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser
355 360 365

Val Leu Gln Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys
370 375 380

Gln Trp Leu Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg
385 390 395 400

Ala Leu Gly Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg
405 410 415

Lys Gly Ala Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu
420 425 430

Gly Lys Thr Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg
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Tyr Phe Glu Leu Arg Gln Gly
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<222> (1)..(25)

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<210> 11
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<220>
<223> Primer sequence

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